

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/529,196A
Source: PU
Date Processed by STIC: 5/24/06

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10/529,196A

CRF Edit Date: 5/24/06
Edited by: JS

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

J Corrected the SEQ ID NO. Sequence numbers edited were:

19

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

___ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

___ Other:



PCT

RAW SEQUENCE LISTING

DATE: 05/24/2006

PATENT APPLICATION: US/10/529,196A

TIME: 11:13:50

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\05242006\J529196A.raw

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3 <110> APPLICANT: Pantherix Limited
4     Primrose, William Ure
5     Ali, Sohail Tahir
6     Maclean, John Kinnaird
8 <120> TITLE OF INVENTION: Crystal Structures of Chorismate Synthase
10 <130> FILE REFERENCE: 7181-1
12 <140> CURRENT APPLICATION NUMBER: US/10/529,196A
C--> 13 <141> CURRENT FILING DATE: 2005-03-24
15 <160> NUMBER OF SEQ ID NOS: 19
17 <170> SOFTWARE: PatentIn version 3.3
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 359
21 <212> TYPE: PRT
22 <213> ORGANISM: Escherichia coli
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26 Ala Gly Asn Thr Ile Gly Gln Leu Phe Arg Val Thr Thr Phe Gly Glu
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30 Ser His Gly Leu Ala Leu Gly Cys Ile Val Asp Gly Val Pro Pro Gly
31           20           25           30
34 Ile Pro Leu Thr Gln Ala Asp Leu Gln His Asp Leu Asp Arg Arg Arg
35           35           40           45
38 Pro Gly Thr Arg Tyr Thr Thr Gln Arg Arg Glu Pro Asp Gln Val Lys
39           50           55           60
42 Ile Leu Ser Gly Val Phe Glu Gly Val Thr Thr Gly Thr Ser Ile Gly
43 65           70           75           80
46 Leu Leu Ile Glu Asn Thr Asp Gln Arg Ser Gln Asp Tyr Ser Ala Ile
47           85           90           95
50 Lys Asp Val Phe Arg Pro Gly His Ala Asp Tyr Thr Tyr Glu Gln Lys
51           100          105          110
54 Tyr Gly Leu Arg Asp Tyr Arg Gly Gly Arg Ser Ser Ala Arg Glu
55           115          120          125
58 Thr Ala Met Arg Val Ala Ala Gly Ala Ile Ala Lys Lys Tyr Leu Ala
59           130          135          140
62 Glu Lys Phe Gly Ile Glu Ile Arg Gly Cys Leu Thr Gln Met Gly Asp
63 145          150          155          160
66 Ile Pro Leu Asp Ile Lys Asp Trp Ser Gln Val Glu Gln Asn Pro Phe
67           165          170          175
70 Phe Cys Pro Asp Pro Asp Lys Ile Asp Ala Leu Asp Glu Leu Met Arg
71           180          185          190
74 Ala Leu Lys Lys Glu Gly Asp Ser Ile Gly Ala Lys Val Thr Val Val
75           195          200          205
78 Ala Ser Gly Val Pro Ala Gly Leu Gly Glu Pro Val Phe Asp Arg Leu
79           210          215          220

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82 Asp Ala Asp Ile Ala His Ala Leu Met Ser Ile Asn Ala Val Lys Gly
83 225                230                235                240
86 Val Glu Ile Gly Asp Gly Phe Asp Val Val Ala Leu Arg Gly Ser Gln
87                245                250                255
90 Asn Arg Asp Glu Ile Thr Lys Asp Gly Phe Gln Ser Asn His Ala Gly
91                260                265                270
94 Gly Ile Leu Gly Gly Ile Ser Ser Gly Gln Gln Ile Ile Ala His Met
95                275                280                285
98 Ala Leu Lys Pro Thr Ser Ser Ile Thr Val Pro Gly Arg Thr Ile Asn
99                290                295                300
102 Arg Phe Gly Glu Glu Val Glu Met Ile Thr Lys Gly Arg His Asp Pro
103 305                310                315                320
106 Cys Val Gly Ile Arg Ala Val Pro Ile Ala Glu Ala Met Leu Ala Ile
107                325                330                335
110 Val Leu Met Asp His Leu Leu Arg Gln Arg Ala Gln Asn Ala Asp Val
111                340                345                350
114 Lys Thr Asp Ile Pro Arg Trp
115                355
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119 <211> LENGTH: 388
120 <212> TYPE: PRT
121 <213> ORGANISM: Streptococcus pneumoniae
123 <400> SEQUENCE: 2
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129 Ile Ile Glu Gly Ile Pro Ala Gly Leu Pro Leu Thr Ala Glu Asp Ile
130                20                25                30
133 Asn Glu Asp Leu Arg Arg Arg Gln Gly Gly Tyr Gly Arg Gly Gly Arg
134                35                40                45
137 Met Lys Ile Glu Asn Asp Gln Val Val Phe Thr Ser Gly Val Arg His
138                50                55                60
141 Gly Lys Thr Thr Gly Ala Pro Ile Thr Met Asp Val Ile Asn Lys Asp
142 65                70                75                80
145 His Gln Lys Trp Leu Asp Ile Met Ser Ala Glu Asp Ile Glu Asp Arg
146                85                90                95
149 Leu Lys Ser Lys Arg Lys Ile Thr His Pro Arg Pro Gly His Ala Asp
150                100               105               110
153 Leu Val Gly Gly Ile Lys Tyr Arg Phe Asp Asp Leu Arg Asn Ser Leu
154                115               120               125
157 Glu Arg Ser Ser Ala Arg Glu Thr Thr Met Arg Val Ala Val Gly Ala
158                130               135               140
161 Val Ala Lys Arg Leu Leu Ala Glu Leu Asp Met Glu Ile Ala Asn His
162 145                150               155               160
165 Val Val Val Phe Gly Gly Lys Glu Ile Asp Val Pro Glu Asn Leu Thr
166                165               170               175
169 Val Ala Glu Ile Lys Gln Arg Ala Ala Gln Ser Glu Val Ser Ile Val
170                180               185               190
173 Asn Gln Glu Arg Glu Gln Glu Ile Lys Asp Tyr Ile Asp Gln Ile Lys
174                195               200               205

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177 Arg Asp Gly Asp Thr Ile Gly Gly Val Val Glu Thr Val Val Gly Gly
178      210      215      220
181 Val Pro Val Gly Leu Gly Ser Tyr Val Gln Trp Asp Arg Lys Leu Asp
182 225      230      235      240
185 Ala Arg Leu Ala Gln Ala Val Val Ser Ile Asn Ala Phe Lys Gly Val
186      245      250      255
189 Glu Phe Gly Leu Gly Phe Glu Ala Gly Tyr Arg Lys Gly Ser Gln Val
190      260      265      270
193 Met Asp Glu Ile Leu Trp Ser Lys Glu Asp Gly Tyr Thr Arg Arg Thr
194      275      280      285
197 Asn Asn Leu Gly Gly Phe Glu Gly Gly Met Thr Asn Gly Gln Pro Ile
198      290      295      300
201 Val Val Arg Gly Val Met Lys Pro Ile Pro Thr Leu Tyr Lys Pro Leu
202 305      310      315      320
205 Met Ser Val Asp Ile Glu Thr His Glu Pro Tyr Lys Ala Thr Val Glu
206      325      330      335
209 Arg Ser Asp Pro Thr Ala Leu Pro Ala Ala Gly Met Val Met Glu Ala
210      340      345      350
213 Val Val Ala Thr Val Leu Ala Gln Glu Ile Leu Glu Lys Phe Ser Ser
214      355      360      365
217 Asp Asn Leu Glu Glu Leu Lys Glu Ala Val Ala Lys His Arg Asp Tyr
218      370      375      380
221 Thr Lys Asn Tyr
222 385
225 <210> SEQ ID NO: 3
226 <211> LENGTH: 388
227 <212> TYPE: PRT
228 <213> ORGANISM: Enterococcus faecalis
230 <400> SEQUENCE: 3
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233 1      5      10      15
236 Ile Ile Glu Gly Leu Pro Ala Gly Leu Pro Leu Ser Ser Glu Glu Ile
237      20      25      30
240 Asn Arg Glu Leu Ala Arg Arg Gln Gly Gly Tyr Gly Arg Gly Gly Arg
241      35      40      45
244 Met Lys Lys Ile Glu Lys Asp Gln Val Arg Ile Thr Ser Gly Ile Arg His
245      50      55      60
248 Gly Lys Thr Leu Gly Ser Pro Val Thr Leu Ile Val Glu Asn Lys Asp
249 65      70      75      80
252 Trp Lys Asn Trp Thr Ser Val Met Ser Val Glu Pro Val Pro Glu Lys
253      85      90      95
256 Gln Lys Lys Ile Arg Arg Val Ser Lys Pro Arg Pro Gly His Ala Asp
257      100      105      110
260 Leu Val Gly Gly Met Lys Tyr Gln His Asp Asp Leu Arg Asn Val Leu
261      115      120      125
264 Glu Arg Ser Ser Ala Arg Glu Thr Thr Met Arg Val Ala Ile Gly Ala
265      130      135      140
268 Val Ala Lys Lys Leu Leu Ala Glu Leu Asp Ile Gln Val Ala Gly His
269 145      150      155      160

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272 Val Ala Val Leu Gly Gly Ile Glu Ala Thr Ile Pro Glu Asn Leu Thr
273           165           170           175
276 Ile Arg Glu Ile Gln Glu Arg Ser Glu Gln Ser Ala Val Arg Val Leu
277           180           185           190
280 Asp Pro Ser Val Glu Glu Lys Met Lys Glu Leu Ile Asp Gln Thr Lys
281           195           200           205
284 Lys Asn Gly Asp Thr Ile Gly Gly Val Val Glu Val Leu Val Gly Gly
285           210           215           220
288 Val Pro Ala Gly Leu Gly Ser Tyr Val Gln Trp Asp Arg Lys Leu Asp
289 225           230           235           240
292 Ala Lys Ile Ala Gln Ala Val Val Ser Ile Asn Ala Phe Thr Gly Ala
293           245           250           255
296 Glu Phe Gly Ile Gly Phe Glu Met Ala Gln Arg Ile Gly Ser Gln Leu
297           260           265           270
300 Met Asp Glu Ile Val Trp Asp Glu Ser Thr Gly Tyr Thr Arg Thr Ser
301           275           280           285
304 Asn Asn Leu Gly Gly Phe Glu Gly Gly Met Thr Asn Gly Met Pro Ile
305           290           295           300
308 Ile Val Arg Gly Val Met Lys Pro Ile Pro Thr Leu Tyr Lys Pro Leu
309 305           310           315           320
312 Gln Ser Val Asn Ile Asp Thr Lys Glu Pro Tyr Lys Ala Ser Val Glu
313           325           330           335
316 Arg Ser Asp Ser Thr Ala Val Pro Ala Ala Ser Val Val Cys Glu Ala
317           340           345           350
320 Val Val Ala Thr Glu Val Ala Lys Ala Met Leu Glu Lys Phe Asp Ser
321           355           360           365
324 Asp Ser Phe Glu Gln Met Lys Glu Ala Val Lys Arg Tyr Arg Leu Tyr
325           370           375           380
328 Thr Gln Asn Phe
329 385
332 <210> SEQ ID NO: 4
333 <211> LENGTH: 388
334 <212> TYPE: PRT.
335 <213> ORGANISM: Staphylococcus aureus
337 <400> SEQUENCE: 4
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340 1           5           10           15
343 Ile Val Glu Gly Val Pro Ala Asn Leu Glu Val Lys Val Glu Asp Ile
344           20           25           30
347 Asn Lys Glu Met Phe Lys Arg Gln Gly Gly Tyr Gly Arg Gly Arg Arg
348           35           40           45
351 Met Gln Ile Glu Lys Asp Thr Val Glu Ile Val Ser Gly Val Arg Asn
352           50           55           60
355 Gly Tyr Thr Leu Gly Ser Pro Ile Thr Met Val Val Thr Asn Asp Asp
356 65           70           75           80
359 Phe Thr His Trp Arg Lys Ile Met Gly Arg Ala Pro Ile Ser Asp Glu
360           85           90           95
363 Glu Arg Glu Asn Met Lys Arg Thr Ile Thr Lys Pro Arg Pro Gly His
364           100           105           110

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367 Ala Asp Leu Leu Gly Gly Met Lys Tyr Asn His Arg Asp Leu Arg Asn
368      115      120      125
371 Val Leu Glu Arg Ser Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Val
372      130      135      140
375 Gly Ala Leu Cys Lys Val Leu Leu Glu Gln Leu Asp Ile Glu Ile Tyr
376 145      150      155      160
379 Ser Arg Val Val Glu Ile Gly Gly Ile Lys Asp Lys Asp Phe Tyr Asp
380      165      170      175
383 Ser Glu Thr Phe Lys Ala Asn Leu Asp Arg Asn Asp Val Arg Val Ile
384      180      185      190
387 Asp Asp Gly Ile Ala Gln Ala Met Arg Asp Lys Ile Asp Glu Ala Lys
388      195      200      205
391 Thr Asp Gly Asp Ser Ile Gly Gly Val Val Gln Val Val Val Glu Asn
392      210      215      220
395 Met Pro Val Gly Val Gly Ser Tyr Val His Tyr Asp Arg Lys Leu Asp
396 225      230      235      240
399 Gly Arg Ile Ala Gln Gly Val Val Ser Ile Asn Ala Phe Lys Gly Val
400      245      250      255
403 Ser Phe Gly Glu Gly Phe Lys Ala Ala Glu Lys Pro Gly Ser Glu Ile
404      260      265      270
407 Gln Asp Glu Ile Leu Tyr Asn Thr Glu Leu Gly Tyr Tyr Arg Gly Ser
408      275      280      285
411 Asn His Leu Gly Gly Leu Glu Gly Gly Met Ser Asn Gly Met Pro Ile
412      290      295      300
415 Ile Val Asn Gly Val Met Lys Pro Ile Pro Thr Leu Tyr Lys Pro Leu
416 305      310      315      320
419 Asn Ser Val Asp Ile Asn Thr Lys Glu Asp Phe Lys Ala Thr Ile Glu
420      325      330      335
423 Arg Ser Asp Ser Cys Ala Val Pro Ala Ala Ser Ile Val Cys Glu His
424      340      345      350
427 Val Val Ala Phe Ala Ile Ala Lys Ala Leu Leu Glu Glu Phe Gln Ser
428      355      360      365
431 Asn His Ile Glu Gln Leu Lys Gln Gln Ile Ile Glu Arg Arg Gln Leu
432      370      375      380
435 Asn Val Glu Phe
436 385
439 <210> SEQ ID NO: 5
440 <211> LENGTH: 368
441 <212> TYPE: PRT
442 <213> ORGANISM: Bacillus subtilis
444 <400> SEQUENCE: 5
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447 1      5      10      15
450 Ile Ile Glu Gly Val Pro Ala Gly Leu Tyr Ile Thr Glu Glu Asp Ile
451      20      25      30
454 Asn Phe Glu Leu Ala Arg Arg Gln Lys Gly His Gly Arg Gly Arg Arg
455      35      40      45
458 Met Gln Ile Glu Lys Asp Gln Ala Lys Ile Met Ser Gly Val Arg His
459      50      55      60

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/529,196A

DATE: 05/24/2006

TIME: 11:13:51

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\05242006\J529196A.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date